

Reference for Transgenic model: Xu et al., Nature Genetics

BASE COUNT

ORIGIN

Query Match

Best local similarity 94.7% Score 17.4; DB 14; Length 165;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 TACCTGAAACAGACGAT 19

DB 6 TACCTGAAACAGACGAT 45

RESULT 9

FEATURES

170 bp mRNA Human EST 29 APR 2000

Accession

Version

KeyWords

Source

Organism

Reference

Authors

Title

Journal

Comment

Source

Features

Base Count

Origin

Query Match

Best local similarity 94.7% Score 17.4; DB 14; Length 170;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 TACCTGAAACAGACGAT 19

DB 148 TACCTGAAACAGACGAT 161

RESULT 10

FEATURES

172 bp mRNA Human EST 19 JAN 2001

Accession

Version

KeyWords

Source

Organism

Reference

Authors

Title

Journal

Comment

Source

Accession
 REF94661 6112285029
 EST
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryotic Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Primates: Catarrhini: Hominoidea: Homo
 1 (bases 1 to 172)

REFERENCE
 AUTHORS
 Liras N, Foz G, Garcia-Correa R, Wajsbom A, Almeida S, Huetos M, Neri M, da Silva W, Jato M, Azeiteiro M, Boudin S, Costa P, Goldanovic H, Carvalheiro A, Miskimmon A, Batael S, Simoes J, Brunstein A, de Oliveira P, Butler P, Invernizzi V, de Brito M, Soares P, Brumatti R, Reis L, de Souza S, and Simpson A

Shed skin sequencing of the human transcriptome with over-expressed sequence tags
 Proc Natl Acad Sci USA 97 (2000) 479-486 (2000)
 20202664

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 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Francisco 100, 4 andar, oficio 419, Sao Paulo, SP, Brazil
 Tel: +55-11 2704922
 Fax: +55-11 2707001

Email: astimpson@ludwig.org.br
 This sequence was derived from the FAIRPLAY Human Cancer Genome Project. This entry can be seen in the following file:
 172 bases (2000-01-19) 172 bases (2000-01-19) 172 bases (2000-01-19)
 172 bases (2000-01-19) 172 bases (2000-01-19) 172 bases (2000-01-19)

Seq primer: pos 16 forward
 High quality sequence: 171
 Location/Qualifiers
 1..172

FEATURES
 SOURCE
 "Homo sapiens"
 "Gene: 9606"
 "Gene: 9606"
 "Gene: 9606"
 "Gene: 9606"

FEATURES
 SOURCE
 "Homo sapiens"
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 "Gene: 9606"
 "Gene: 9606"

[illegible]

for identifying expressed genes. (1) is useful in gene therapy techniques
 to restore normal activity of (1) or to treat disease states. The term
 (11) (11) is useful for generating antibodies against it, detection of
 or quantitating a polypeptide in tissue, as molecular weight markers and as
 a food supplement. (11) and its binding partners are useful in medical
 treatment of stress expression (11) - (1) and (11) are useful for treatment
 of disorders involving abnormal protein expression or biochemical activity.
 The polypeptide and polynucleotide sequences have applications in
 diagnosis, forensics, gene mapping, identification of mutations
 or response to gene therapy disorders or other traits and to assess
 or to produce other types of data and products dependent on DNA and
 or amino acid sequences. AAS9464 AAS9464 represent novel human
 or diagnostic coding sequences of the invention.
 or Note: The sequence data for this patent did not appear in the printed
 or specification, but was obtained in electronic format directly from Wipo
 or at <http://wipo.int/Pub/Publicat/pubseq.asp>.

Sequence: 100 bp: 27 A: 5' 3' 4' 5' 6' 7' 8' 9' 10' 11' 12' 13' 14' 15' 16' 17' 18' 19' 20' 21' 22' 23' 24' 25' 26' 27' 28' 29' 30' 31' 32' 33' 34' 35' 36' 37' 38' 39' 40' 41' 42' 43' 44' 45' 46' 47' 48' 49' 50' 51' 52' 53' 54' 55' 56' 57' 58' 59' 60' 61' 62' 63' 64' 65' 66' 67' 68' 69' 70' 71' 72' 73' 74' 75' 76' 77' 78' 79' 80' 81' 82' 83' 84' 85' 86' 87' 88' 89' 90' 91' 92' 93' 94' 95' 96' 97' 98' 99' 100' 101' 102' 103' 104' 105' 106' 107' 108' 109' 110' 111' 112' 113' 114' 115' 116' 117' 118' 119' 120' 121' 122' 123' 124' 125' 126' 127' 128' 129' 130' 131' 132' 133' 134' 135' 136' 137' 138' 139' 140' 141' 142' 143' 144' 145' 146' 147' 148' 149' 150' 151' 152' 153' 154' 155' 156' 157' 158' 159' 160' 161' 162' 163' 164' 165' 166' 167' 168' 169' 170' 171' 172' 173' 174' 175' 176' 177' 178' 179' 180' 181' 182' 183' 184' 185' 186' 187' 188' 189' 190' 191' 192' 193' 194' 195' 196' 197' 198' 199' 200' 201' 202' 203' 204' 205' 206' 207' 208' 209' 210' 211' 212' 213' 214' 215' 216' 217' 218' 219' 220' 221' 222' 223' 224' 225' 226' 227' 228' 229' 230' 231' 232' 233' 234' 235' 236' 237' 238' 239' 240' 241' 242' 243' 244' 245' 246' 247' 248' 249' 250' 251' 252' 253' 254' 255' 256' 257' 258' 259' 260' 261' 262' 263' 264' 265' 266' 267' 268' 269' 270' 271' 272' 273' 274' 275' 276' 277' 278' 279' 280' 281' 282' 283' 284' 285' 286' 287' 288' 289' 290' 291' 292' 293' 294' 295' 296' 297' 298' 299' 300' 301' 302' 303' 304' 305' 306' 307' 308' 309' 310' 311' 312' 313' 314' 315' 316' 317' 318' 319' 320' 321' 322' 323' 324' 325' 326' 327' 328' 329' 330' 331' 332' 333' 334' 335' 336' 337' 338' 339' 340' 341' 342' 343' 344' 345' 346' 347' 348' 349' 350' 351' 352' 353' 354' 355' 356' 357' 358' 359' 360' 361' 362' 363' 364' 365' 366' 367' 368' 369' 370' 371' 372' 373' 374' 375' 376' 377' 378' 379' 380' 381' 382' 383' 384' 385' 386' 387' 388' 389' 390' 391' 392' 393' 394' 395' 396' 397' 398' 399' 400' 401' 402' 403' 404' 405' 406' 407' 408' 409' 410' 411' 412' 413' 414' 415' 416' 417' 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1845' 1846' 1847' 1848' 1849' 1850' 1851' 1852' 1853' 1854' 1855' 1856' 1857' 1858' 1859' 1860' 1861' 1862' 1863' 1864' 1865' 1866' 1867' 1868' 1869' 1870' 1871' 1872' 1873' 1874' 1875' 1876' 1877' 1878' 1879' 1880' 1881' 1882' 1883' 1884' 1885' 1886' 1887' 1888' 1889' 1890' 1891' 1892' 1893' 1894' 1895' 1896' 1897' 1898' 1899' 1900' 1901' 1902' 1903' 1904' 1905' 1906' 1907' 1908' 1909' 1910' 1911' 1912' 1913' 1914' 1915' 1916' 1917' 1918' 1919' 1920' 1921' 1922' 1923' 1924' 1925' 1926' 1927' 1928' 1929' 1930' 1931' 1932' 1933' 1934' 1935' 1936' 1937' 1938' 1939' 1940' 1941' 1942' 1943' 1944' 1945' 1946' 1947' 1948' 1949' 1950' 1951' 1952' 1953' 1954' 1955' 1956' 1957' 1958' 1959' 1960' 1961' 1962' 1963' 1964' 1965' 1966' 1967' 1968' 1969' 1970' 1971' 1972' 1973' 1974' 1975' 1976' 1977' 1978' 1979' 1980' 1981' 1982' 1983' 1984' 1985' 1986' 1987' 1988' 1989' 1990' 1991' 1992' 1993' 1994' 1995' 1996' 1997' 1998' 1999' 2000' 2001' 2002' 2003' 2004' 2005' 2006' 2007' 2008' 2009' 2010' 2011' 2012' 2013' 2014' 2015' 2016' 2017' 2018' 2019' 2020' 2021' 2022' 2023' 2024' 2025' 2026' 2027' 2028' 2029' 2030' 2031' 2032' 2033' 2034' 2035' 2036' 2037' 2038' 2039' 2040' 2041' 2042' 2043' 2044' 2045' 2046' 2047' 2048' 2049' 2050' 2051' 2052' 2053' 2054' 2055' 2056' 2057' 2058' 2059' 2060' 2061' 2062' 2063' 2064' 2065' 2066' 2067' 2068' 2069' 2070' 2071' 2072' 2073' 2074' 2075' 2076' 2077' 2078' 2079' 2080' 2081' 2082' 2083' 2084' 2085' 2086' 2087' 2088' 2089' 2090' 2091' 2092' 2093' 2094' 2095' 2096' 2097' 2098' 2099' 2100' 2101' 2102' 2103' 2104' 2105' 2106' 2107' 2108' 2109' 2110' 2111' 2112' 2113' 2114' 2115' 2116' 2117' 2118' 2119' 2120' 2121' 2122' 2123' 2124' 2125' 2126' 2127' 2128' 2129' 2130' 2131' 2132' 2133' 2134' 2135' 2136' 2137' 2138' 2139' 2140' 2141' 2142' 2143' 2144' 2145' 2146' 2147' 2148' 2149' 2150' 2151' 2152' 2153' 2154' 2155' 2156' 2157' 2158' 2159' 2160' 2161' 2162' 2163' 2164' 2165' 2166' 2167' 21


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XX  US6104465.A.
XX
XX  15-AUG-2000.
XX
XX  03-OCT-1995: 9508-0538666.
XX
XX  14-FEB-1995: 9508-0390251.
XX
XX  (PEER ) PEEKIN ELMER C&P.
XX
XX  Partam P., Johnston low L., Chadwick BP.
XX
XX  WPI: 2000-54254/49.
XX
XX  Typing HLA class I genes for organ transplantation involves comparing
XX  the sample DNA containing HLA class I gene comprising two exons and a
XX  target sequence, with amplification primers and detecting the amplicon
XX
XX  Example 2: Fig 11: 60pp; English.
XX
XX  The present sequence is over 2 of Human leukocyte Antigen-B (HLA-B) gene.
XX  HLA-B gene is found on chromosome 6p21.3. HLA class I proteins are found
XX  on the surface of almost all nucleated cells and are involved in antigen
XX  presentation to immune system cells. This sequence was used in the method
XX  of the present invention, in which primers are used to type HLA class I
XX  genes by carrying out PCR on a sample DNA, comprising HLA class I gene,
XX  and detecting the amplicon formed using a sequence-specific detection
XX  method e.g. DNA sequencing. The method of the present invention is useful
XX  for discriminating among the HLA-A, HLA-B, and HLA-C genes and other
XX  related class I genes and pseudogenes. In addition, the method of the
XX  present invention is useful for organ transplantation studies, for the
XX  study of autoimmune disease and for the determination of susceptibility
XX  to infectious disease.
XX
XX  Sequence 270 bp: 50 A: 85 G: 90 C: 35 T: 0 other:
XX
XX  Query Match 91.6% Score 17.41 Db 21: Length 270
XX  Best Local Similarity 94.7% Prod. No. 20:
XX  Matches 16: conservative 0: Mismatches 1: Indels 0: Gaps 0:
XX
XX  1 TACGTGACACACACACACT 19
XX  |||||
XX  79 TACGTGACACACACACT 97
XX
XX  RESULT 9
XX  AAA04615
XX  ID AAA04615 standard: DNA, 270 bp.
XX
XX  AAA04615:
XX
XX  11 JAN 2001 (first entry)
XX
XX  HLA-C gene exon 2 #1.
XX
XX  Human leukocyte Antigen HLA-C gene product of the HLA class I
XX  organ transplantation autoimmune disease
XX  Involving disease entry: 1161117, chromosome 6p21.3, loc.
XX
XX  Homo sapiens.
XX
XX  OS:104465.A.
XX
XX  15 AUG-2000.
XX
XX  03-OCT-1995: 9508-0538666.
XX
XX  14-FEB-1995: 9508-0390251.
XX
XX  (PEER ) PEEKIN ELMER C&P.
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XX  Partam P., Johnston-low L., Chadwick BP.
XX
XX  WPI: 2000 54254/49.
XX
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XX  on the surface of almost all nucleated cells and are involved in antigen
XX  presentation to immune system cells. This sequence was used in the method
XX  of the present invention, in which primers are used to type HLA class I
XX  genes by carrying out PCR on a sample DNA, comprising HLA class I gene,
XX  and detecting the amplicon formed using a sequence-specific detection
XX  method e.g. DNA sequencing. The method of the present invention is useful
XX  for discriminating among the HLA-A, HLA-B, and HLA-C genes and other
XX  related class I genes and pseudogenes. In addition, the method of the
XX  present invention is useful for organ transplantation studies, for the
XX  study of autoimmune disease and for the determination of susceptibility
XX  to infectious disease.
XX
XX  Sequence 270 bp: 54 A: 85 G: 99 C: 34 T: 0 other:
XX
XX  Query Match 91.6% Score 17.41 Db 21: Length 270
XX  Best Local Similarity 94.7% Prod. No. 20:
XX  Matches 16: conservative 0: Mismatches 1: Indels 0: Gaps 0:
XX
XX  1 TACGTGACACACACACT 19
XX  |||||
XX  78 TACGTGACACACACT 96
XX
XX  RESULT 10
XX  AAA11077
XX  ID AAA11077 standard: DNA, 270 bp.
XX
XX  AAA11077:
XX
XX  28-JUL-2000 (first entry)
XX
XX  Consensus sequence for exon 2 of non-classical HLA genes.
XX
XX  Tissue sample testing: allelic typing human leukocyte antigen
XX  PCR primer: probe: hybridisation: intron: amplification: ds:
XX  allelic variation: non-classical HLA class I genes exon.
XX
XX  Homo sapiens.
XX
XX  OS6010775.A.
XX
XX  29-FEB-2000.
XX
XX  22-JUN-1995: 9508-0577081.
XX
XX  22-JUN-1995: 9508-0577081.
XX
XX  (PEER ) CHINESE R.
XX  (TAN) Y. YAN S Y.
XX
XX  Corob N., Yama SY.
XX
XX  WPI: 2000 224159/19.
XX
XX  Testing a tissue sample to determine the allelic type of a human
XX  leukocyte antigen class I gene involves amplifying two exons and a
XX  polymers with primers which flank a region including an allelic
XX  variation of the HLA class I gene.
XX
XX  Disclosure: column 51-52: 90pp; English.
XX

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICANT NUMBER: 95/04127,954
  FILING DATE:
  CLASSIFICATION: 436
  ATTORNEY/AGENT INFORMATION:
    NAME: Petty, Douglas A.
    REGISTRATION NUMBER: 45,421
    REFERENCE/CHECK NUMBER: 8671
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (510) 814-2974
    TELEFAX: (510) 814-2977
  INFORMATION FOR SEQ ID NO: 62:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 270 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
  US-08 127-954-62

Query Match
  Best Local Similarity: 94.78; Score 17.4; 100%; Length 270;
  Matches: 100 Conservative 0; Mismatches 1; Gaps 0;

CY 1 TACCTGCAACACACGACAT 19
100 11111111111111111111
100 78 TACCTGCAACACACGACAT 96

RESULT 11
US-08 127-954-63
Sequence 63, Application US/08127954
Patent No. 5451512
GENERAL INFORMATION:
  APPLICANT: Apple, Raymond J.
  ATTORNEY/AGENT INFORMATION:
    NAME: Petty, Douglas A.
    REGISTRATION NUMBER: 45,421
    REFERENCE/CHECK NUMBER: 8674
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (510) 814-2974
    TELEFAX: (510) 814-2977
  INFORMATION FOR SEQ ID NO: 63:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 270 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
  US-08 127-954-63

Query Match
  Best Local Similarity: 94.78; Score 17.4; 100%; Length 270;
  Matches: 100 Conservative 0; Mismatches 1; Gaps 0;

CY 1 TACCTGCAACACACGACAT 19
100 11111111111111111111
100 78 TACCTGCAACACACGACAT 96

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US-08 127-954-64
Query Match
  Best Local Similarity: 94.78; Score 17.4; 100%; Length 270;
  Matches: 100 Conservative 0; Mismatches 1; Gaps 0;

CY 1 TACCTGCAACACACGACAT 19
100 11111111111111111111
100 78 TACCTGCAACACACGACAT 96

RESULT 12
US-08 127-954-64
Sequence 64, Application US/08127954
Patent No. 5451512
GENERAL INFORMATION:
  APPLICANT: Apple, Raymond J.
  ATTORNEY/AGENT INFORMATION:
    NAME: Petty, Douglas A.
    REGISTRATION NUMBER: 45,421
    REFERENCE/CHECK NUMBER: 8674
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (510) 814-2974
    TELEFAX: (510) 814-2977
  INFORMATION FOR SEQ ID NO: 64:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 270 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
  US-08 127-954-64

Query Match
  Best Local Similarity: 94.78; Score 17.4; 100%; Length 270;
  Matches: 100 Conservative 0; Mismatches 1; Gaps 0;

CY 1 TACCTGCAACACACGACAT 19
100 11111111111111111111
100 78 TACCTGCAACACACGACAT 96

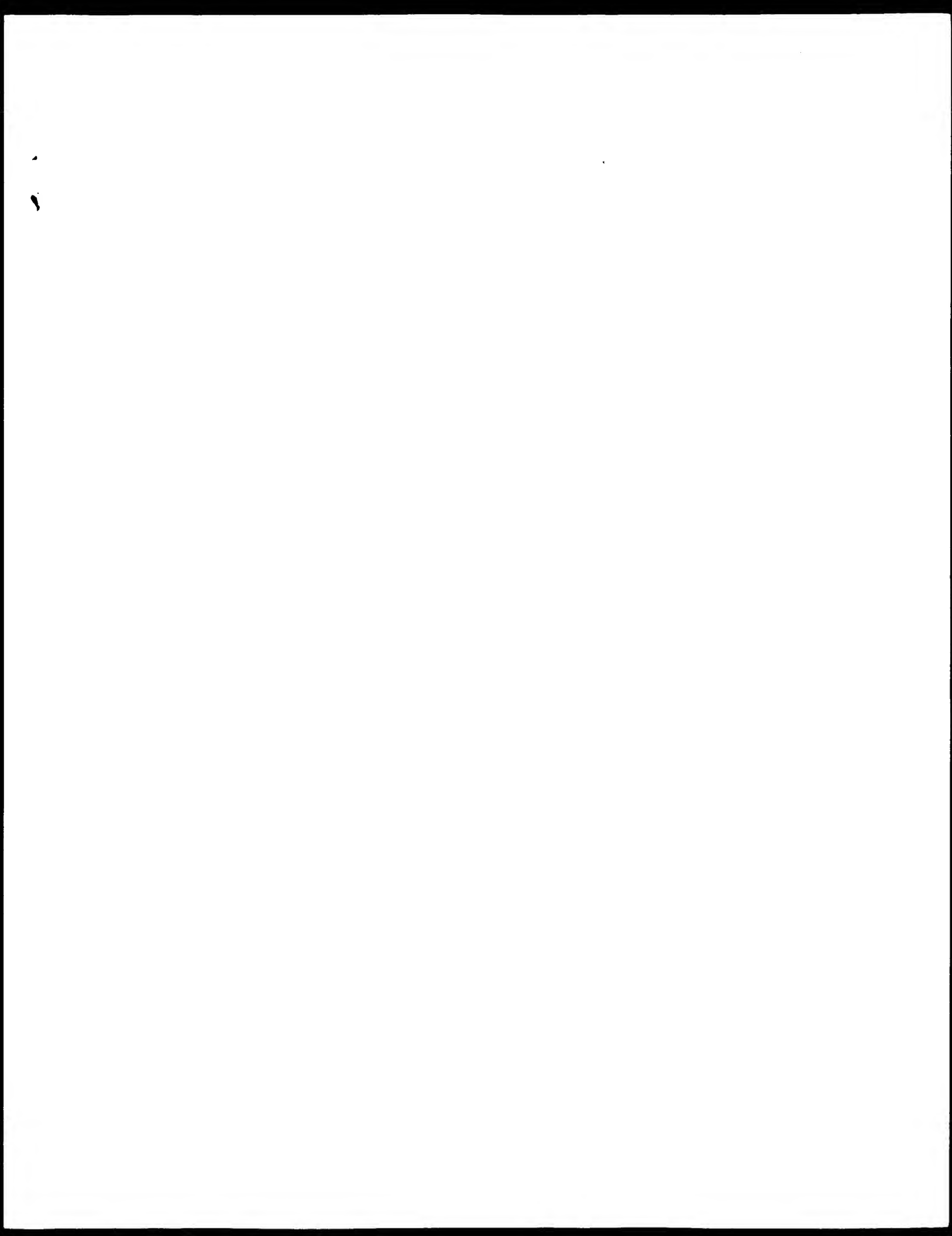
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Tue Apr 15 15:22:38 2003

us-09-856-662-3.mri

Page 7

Search completed: April 15, 2003, 01:45:41
Job time : 90 secs



FILE REFERENCE: 2101-01-11
 CURRENT APPLICATION NUMBER: 2579/220,455
 CURRENT FILING DATE: 2001-08-01
 NUMBER OF SEQ ID NOS: 275
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 205
 LENGTH: 495
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc-feature
 LOCATION: 378..379..398
 OTHER INFORMATION: n = A, L, C or T
 US 09-856-662-3

Query Match 91.4% Score 17.4; DB 10; Length 422;
 Best Local Similarity 94.7% Pred. No. 4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 1 TACGIGGACAAACGACG 19
 14 157 TACGIGGACAAACGACG 175

RESULT 6

US 09-856-662-3
 Sequence 6792 Application US 09-856-662-3
 Patent No. US 20020147139A1
 GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
 APPLICANT: Jac, Neelam
 APPLICANT: Hyatt, John C.
 APPLICANT: Mathialagan, Narayanan
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 FILE REFERENCE: 16511006/77 2101029892
 CURRENT APPLICATION NUMBER: US 2002/09-856-662
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 9792
 LENGTH: 422
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: N. C. 12 LER 08 011 11 11 11
 US 09-856-662-3

Query Match 91.4% Score 17.4; DB 10; Length 422;
 Best Local Similarity 94.7% Pred. No. 4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 1 TACGIGGACAAACGACG 19
 14 149 TACGIGGACAAACGACG 167

RESULT 7

US 09-856-662-3
 Sequence 2127 Application US 09-856-662-3
 Patent No. US 20020147139A1
 GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
 APPLICANT: Jac, Neelam
 APPLICANT: Hyatt, John C.
 APPLICANT: Mathialagan, Narayanan
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 FILE REFERENCE: 16511006/77 2101029892
 CURRENT APPLICATION NUMBER: US 2002/09-856-662
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 2127
 LENGTH: 429
 TYPE: DNA

ORGANISM: Bos taurus
 OTHER INFORMATION: N. C. 12 LER 08 011 11 11 11
 US 09-856-662-3

Query Match 91.4% Score 17.4; DB 10; Length 422;
 Best Local Similarity 94.7% Pred. No. 4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 1 TACGIGGACAAACGACG 19
 14 255 TACGIGGACAAACGACG 250

RESULT 8

US 09-856-662-3
 Sequence 739 Application US 09-856-662-3
 Patent No. US 20020147139A1
 GENERAL INFORMATION:
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 FILE REFERENCE: 16511006/77 2101029892
 CURRENT APPLICATION NUMBER: US 2002/09-856-662
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 739
 LENGTH: 422
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: N. C. 12 LER 08 011 11 11 11
 US 09-856-662-3

Query Match 91.4% Score 17.4; DB 10; Length 422;
 Best Local Similarity 94.7% Pred. No. 4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 1 TACGIGGACAAACGACG 19
 14 157 TACGIGGACAAACGACG 175

RESULT 9

US 09-856-662-3
 Sequence 739 Application US 09-856-662-3
 Patent No. US 20020147139A1
 GENERAL INFORMATION:
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 FILE REFERENCE: 16511006/77 2101029892
 CURRENT APPLICATION NUMBER: US 2002/09-856-662
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 739
 LENGTH: 422
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: N. C. 12 LER 08 011 11 11 11
 US 09-856-662-3

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 Best Local Similarity 94.7% Pred. No. 4;
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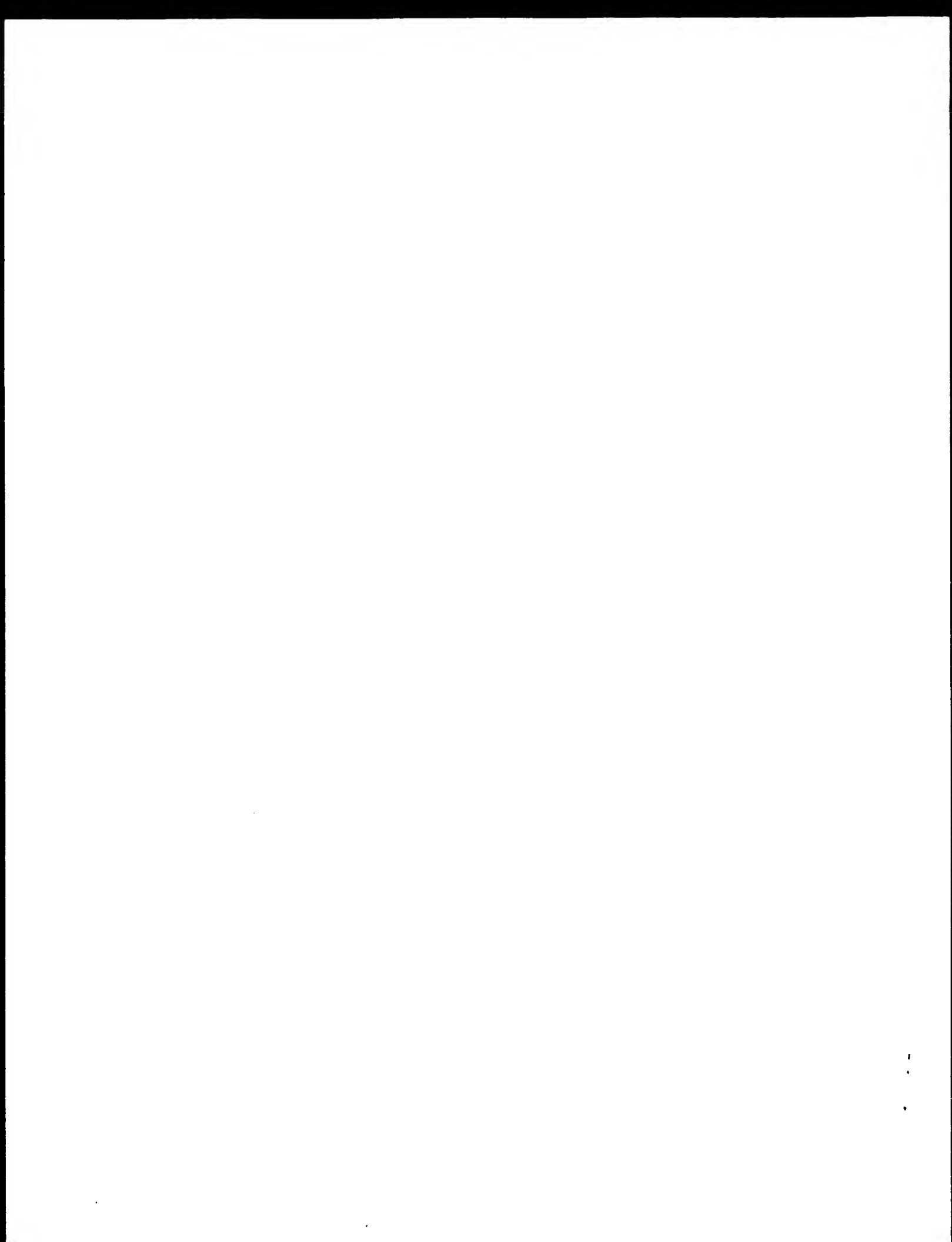
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 14 157 TACGIGGACAAACGACG 175

RESULT 10

US 09-856-662-3
 Sequence 739 Application US 09-856-662-3
 Patent No. US 20020147139A1
 GENERAL INFORMATION:
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 TITLE OF INVENTION: HUSKLE AND FAT DEPOSITION
 FILE REFERENCE: 16511006/77 2101029892
 CURRENT APPLICATION NUMBER: US 2002/09-856-662
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 739
 LENGTH: 422
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: N. C. 12 LER 08 011 11 11 11
 US 09-856-662-3

Query Match 91.4% Score 17.4; DB 10; Length 422;
 Best Local Similarity 94.7% Pred. No. 4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 1 TACGIGGACAAACGACG 19
 14 157 TACGIGGACAAACGACG 175




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QY 1 TAGTGAGCAAAACAGCAGT 19
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PB 127 TAGTGAGCAAAACAGCAGT 145

RESULT 5
AF179648
LOCUS
DEFINITION
  1092 bp. mRNA. linear. PRI 19 JUN 2000
  Pan troglodytes MHC class I antigen (Patr A) mRNA, full: A*0802
  allele, partial cds.
ACCESSION
  AF179648
VERSION
  AF179648.1 GI:8571964
KEYWORDS
  Source
  Pan troglodytes.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
  1 (bases 1 to 1092)
  Adams,E.J., Cooper,S., Thomson,G., and Parham,P.
  Common chimpanzees have greater diversity than humans at two of the
  three highly polymorphic MHC class I genes
  Immunogenetics 51 (6), 410-424 (2000)
JOURNAL
  2322476
MEDLINE
  10866107
PUBMED
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REFERENCE
  2 (bases 1 to 1092)
  Adams,E.J., Cooper,S., Thomson,G., and Parham,P.
  Direct Submission
  Submitted (24 Apr 1999) Structural Biology (Structural/Integrative
  Biology) (UC Berkeley), Structural Biology, 601 Pilsbury Hall,
  1110 West, Stanford, CA 94305, USA
JOURNAL
  Immunogenetics 51 (6), 410-424 (2000)
MEDLINE
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PUBMED
  10866107
REFERENCE
  2 (bases 1 to 1092)
  Adams,E.J., Cooper,S., Thomson,G., and Parham,P.
  Direct Submission
  Submitted (24 Apr 1999) Structural Biology (Structural/Integrative
  Biology) (UC Berkeley), Structural Biology, 601 Pilsbury Hall,
  1110 West, Stanford, CA 94305, USA
JOURNAL
  Immunogenetics 51 (6), 410-424 (2000)
MEDLINE
  2322476
PUBMED
  10866107
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Query Match
  Best Local Similarity 100.0%; Score 19; DB 9; Length 1092;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGTGAGCAAAACAGCAGT 19
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PB 145 TAGTGAGCAAAACAGCAGT 164

RESULT 11
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LOCUS
DEFINITION
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  Pan troglodytes MHC class I antigen (Patr A) mRNA, full: A*0801
  allele, complete cds.
ACCESSION
  AF168404
VERSION
  AF168404.1 GI:81173418
KEYWORDS
  Source
  Pan troglodytes.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
  1 (bases 1 to 1098)
  de Groot,N.G., Orlow,N., Asquith,K., Watkins,D.L., Lockhart,D.G.,
  Madrigal,J.A., and Bontrop,K.E.
  Major histocompatibility complex class I diversity in a West
  African chimpanzee population: implications for HIV research
  Immunogenetics 51 (6), 396-409 (2000)
JOURNAL
  20322475
MEDLINE
  10866106
PUBMED
  10866106
REFERENCE
  2 (bases 1 to 1098)
  de Groot,N.G., Orlow,N., Asquith,K., Watkins,D.L., Lockhart,D.G.,
  Madrigal,J.A., and Bontrop,K.E.

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